

## Leukaemia Section

### Mini Review

# t(11;16)(q23;p13.3)

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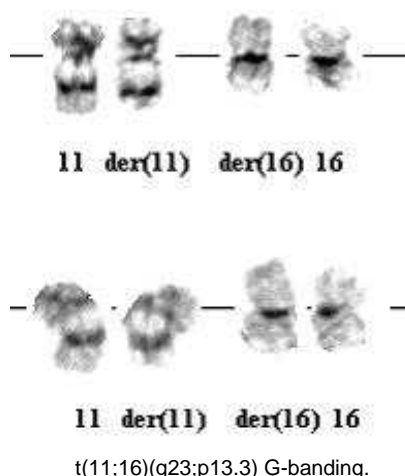
Online updated version: <http://AtlasGeneticsOncology.org/Anomalies/t1116q23p13ID1120.html>

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### Identity



### Clinics and pathology

#### Disease

Treatment-related myelodysplastic syndrome (t-MDS) or treatment-related acute leukaemia, usually myeloblastic (t-AML), less often lymphoblastic (t-ALL).

Two case reports describe a de novo leukaemia with t(11;16)(q23;p13.3): an AML-M4 (Glassman et al., 2003) and an infant ALL, which switch into AML with retention of the translocation (Stasik et al., 2006).

#### Phenotype/cell stem origin

Variable phenotypes: most often LAM4 in t-AML (but also LAM5a and LAM2); chronic myelomonocytic leukaemia (CMML) in t-MDS.

#### Etiology

Chemotherapy for other primary malignancies (including leukaemia, lymphoma and solid tumors) using topoisomerase II inhibitors (epipodophyllo-toxins or anthracyclins).

#### Epidemiology

Rare translocation (about twenty cases described), found at any age, from infancy to elder age.

#### Prognosis

Poor, as in other therapy-related leukaemia.

### Cytogenetics

#### Cytogenetics morphological

Can be seen with G-banding: chromosome 11 appears shortened, chromosome 16 enlarged (11q- and 16p+).

#### Cytogenetics molecular

FISH may be needed.

#### Additional anomalies

In half cases about, no recurrent additional cytogenetic anomalies.

### Genes involved and proteins

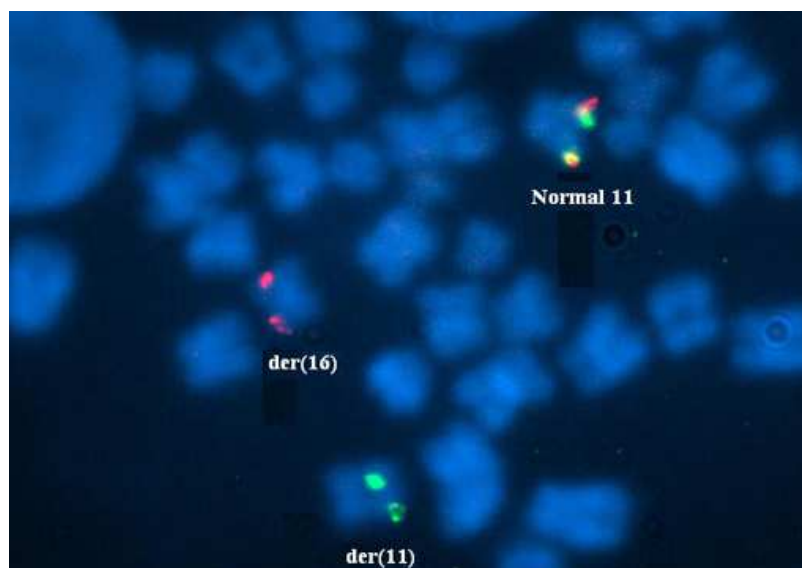
#### MLL

##### Location

11q23

##### DNA/RNA

37 exons, spanning over 100 kb.



Fish studies using a commercially available MLL break-apart probe (Vysis® LSI® MLL Dual Color). The derivative 11 shows a single green signal indicating rearrangement of the MLL locus. The derivative 16 has the translocated portion of the MLL indicated by a single red signal.

### Protein

MLL is a "multipartner" gene involved in multiple rearrangements: the most frequent partners are AF4 in 4q21, AF6 in 6q27, AF9 in 9p22, ELL in 19p13.1 and ENL in 19p13.3.

MLL is a major regulator of hematopoiesis and embryonic development, through HOX genes expression regulation. MLL binds to promoters of HOX genes such as Hoxa7 and Hoxa9 (proteins which regulate hematopoiesis and are normally expressed only in early hematopoietic progenitors) through acetylation and methylation of histones.

### CBP (CREB-binding protein)

#### Location

16p13.3

#### DNA/RNA

About 154 kb, 32 exons.

### Protein

It is a transcriptional coactivator involved in coordinating signal from many sequence-specific activators to modulate transcription and/or cell cycle progression. It has endogenous histone acetyltransferase activity and may contribute to transcriptional regulation via targeted acetylation of chromatin.

## Result of the chromosomal anomaly

### Hybrid gene

#### Transcript

5' MLL - 3' CBP on the der(11) and 5' CBP - 3' MLL on the der(16).

Variable breakpoints: In MLL, almost all of the

breakpoints occurs in an 8.3-kb fragment known as the breakpoint cluster region (BCR), encompassing exons 8-14. In CBP, the genomic breakpoints clustered in an 8.2-kb region of intron 3 (BCR 8.2kb), which is different of the breakpoints in CBP for patients with t(8;16) clustered in a 2.3-kb region in intron 2 (BCR 2.3kb).

### Fusion protein

#### Description

N-Term from MLL (containing the AT-hooks and repression domain) fused to the C-Term of CBP (almost always including the CREB binding domain, bromodomain, histone acetyltransferase domain).

## References

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